

Familial Adenomatous Polyposis | Cancer Institute NSW

<https://www.cancer.nsw.gov.au/what-we-do/...>

Familial Adenomatous Polyposis (FAP) is caused by a change (mutation) in the APC gene. Everyone has two copies of the APC gene, but people with FAP have one working copy and one non-working copy.

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Author: Jingyun Li, Rui Wang, Xin Zhou, Wendon...

Publish Year: 2020

The Intestinal Microbiota and Colorectal Cancer - Frontiers

<https://www.frontiersin.org/articles/10.3389/fimmu.2020.615056>

Nov 30, 2020 · Evidence from twin and family studies indicates that only a small fraction of CRCs, including familial adenomatous polyposis (FAP), hereditary nonpolyposis colorectal cancer (HNPCC or...

Author: Yiwen Cheng, Zongxin Ling, Lanjuan Li Publish Year: 2020

New insights into POLE and POLD1 germline mutations in ...

<https://academic.oup.com/hmg/article-abstract/23/13/3506/660575>

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2. Hereditary and Sporadic Colorectal Cancer and Their Link to the Human Gut Microbiota The Knudson's classic two-hit model was hypothesized to explain CRC carcinogenesis and it seems to be...

Author: Giorgia Mori, Maria Rosalia Pasca Publish Year: 2021

Diet, Microbiota, and Colorectal Cancer - ScienceDirect

<https://www.sciencedirect.com/science/article/pii/S2589004219303906>

Nov 22, 2019 · However, recent evidences have shown that the progression from polyp to cancer involves not only the accumulation of multiple mutations, but also alteration at different molecular events (Lao a...

Changes of Gut Microbiota in Fap and UC Patients in ...

<https://www.preprints.org/manuscript/202012.0416/v1> ▾

Inflammatory bowel diseases, familial adenomatous polyposis (FAP) and colorectal cancer (CRC) are associated with alterations of the intestinal microbiota. However, few data are available on the perpetuation of FAP and ulcerative colitis (UC) in relation to microbial dysbiosis. This study evaluated the UC and genetically confirmed FAP patients' gut microbial balance in concordance to clinical outcome.

[PDF] Gut Microbial Signatures in Sporadic and Hereditary ...

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The second most common hereditary syndrome is the **familial adenomatous polyposis (FAP)** and its variants (Gardner syndrome, Turcot syndrome, and attenuated FAP), which account for less than 1% of CRCs. FAP is caused by germline mutations in the **adenomatous polyposis coli (APC)** gene which is located on chromosome 5. In typical FAP, numerous

Author: Giorgia Mori, Maria Rosalia Pasca **Publish Year:** 2021

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- How is familial adenomatous polyposis (APC) related to APC? ▾
- How are adenomas and carcinomas obtained from FAPs? ▾
- How is the gut microbiota related to colorectal neoplasia? ▾

Name of Journal: *World Journal of Gastrointestinal Oncology*

Manuscript NO: 64580

Manuscript Type: REVIEW

Familial adenomatous polyposis and changes in the gut microbiota: new insights into colorectal cancer carcinogenesis

Familial adenomatous polyposis and microbiota

Abstract

Patients with familial adenomatous polyposis, an autosomal dominant hereditary colorectal cancer syndrome, show a lifetime risk of developing cancer close to 100%. Recent studies have pointed out that the gut microbiota could play a crucial role in the development of colorectal adenomas and the consequent progression to colorectal cancer. Some gut bacteria, such as *Fusobacterium nucleatum*, *Escherichia coli*, *Clostridium difficile*, *Peptostreptococcus* and enterotoxigenic *Bacteroides fragilis*, could be implicated in colorectal carcinogenesis through different mechanisms, including the maintenance

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Familial adenomatous polyposis and changes in the gut microbiota:



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The second most common hereditary syndrome is the **familial adenomatous polyposis (FAP)** and its variants (Gardner syndrome, Turcot syndrome, and attenuated FAP), which account for less than 1% of CRCs. FAP is caused by germline mutations in the **adenomatous polyposis coli (APC)** gene which is located on chromosome 5. In typical FAP, numerous

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PEOPLE ALSO ASK

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How is familial adenomatous polyposis (APC) related to APC? ▾

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Feedback

[Molecular nature of colon tumors in hereditary ...](#)

<https://www.ncbi.nlm.nih.gov/pubmed/8690195>

To clarify the nature of HNPCC tumors, RER and genetic **changes** were compared between HNPCC and non-HNPCC tumors. METHODS: RER and genetic **changes** were analyzed in 21 HNPCC, 389 **familial adenomatous polyposis**, and 206 sporadic tumors using polymerase chain reaction, single-strand conformation polymorphism, sequencing, and Southern hybridization.

Cited by: 645 Author: M Konishi, R Kikuchi-Yanoshita, K Tanak...

Publish Year: 1996